

What is claimed is:

1. A method to infer breed of a bovine subject from a nucleic acid sample of the bovine subject, comprising identifying in the nucleic acid sample, at least one nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with a breed, thereby inferring the breed of the bovine subject.
2. The method of claim 1, wherein the nucleotide occurrence of at least 2 of the SNPs is determined to infer the breed.
3. The method of claim 2, wherein the nucleotide occurrences of the at least 2 SNPs comprise a haplotype allele, and wherein the method infers the breed using the identified haplotype allele.
4. The method of claim 3, further comprising identifying a diploid pair of haplotype alleles and inferring the breed using the diploid pair of haplotype alleles.
5. The method of claim 1, wherein the identified nucleotide occurrence is associated with Angus, Holstein, Limousin, Brahman, Simmental, Hereford, Gelbvieh or Charolais cattle.
6. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Angus cattle is identified.
7. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Brahman cattle is identified.
8. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Limousin cattle is identified.

9. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Simmental cattle is identified.

10. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Hereford cattle is identified.

11. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Charolais cattle is identified.

12. The method of claim 5, wherein at least one nucleotide occurrence of at least one SNP listed in Table 5 or Table 3A as associated with Gelbvieh cattle is identified.

13. The method of claim 1, further comprising marketing the subject prior to harvest based on the inferred breed.

14. The method of claim 1, further comprising managing the subject in the feedlot to obtain improved performance based on known characteristics of the inferred breed for the subject.

15. The method of claim 1, further comprising identifying a nucleotide sequence of a hypermutable sequence in the sample, and inferring breed based on the at least one nucleotide occurrence and the nucleotide sequence of the hypermutable sequence.

16. The method of claim 1, further comprising marketing a product of the bovine subject based on the inferred breed.

17. The method of claim 16, wherein the marketing of the product comprises marketing the product under a trademark specific for a breed.

18. A method for determining a nucleotide occurrence of a single nucleotide polymorphism (SNP) in a bovine sample, comprising:

a) contacting a bovine polynucleotide in the sample with an oligonucleotide that binds to a target region of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895; and

b) determining the nucleotide occurrence of a single nucleotide polymorphism (SNP) corresponding to position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the determination comprises analyzing binding of the oligonucleotide, or detecting an amplification product generated using the oligonucleotide, thereby determining the nucleotide occurrence of the SNP.

19. The method of claim 18, wherein the oligonucleotide binds to a target sequence that comprises one of the SNPs, and the nucleotide occurrence is determined based on the binding of the oligonucleotide to the target sequence.

20. The method of claim 18, wherein the bovine polynucleotide is contacted with a pair of oligonucleotides that comprise a primer pair, and the nucleotide occurrence is determined using an amplification product generated using the primer pair.

21. The method of claim 20, wherein at least one primer of the primer pair is any one of SEQ ID NOS:Forward1 to Reverse4868.

22. The method of claim 21, wherein the primer pair is any of the forward and reverse primer pairs listed in Table 6.

23. The method of claim 19, wherein the terminal nucleotide of the oligonucleotide binds to the SNP.

24. The method of claim 23, wherein the method comprises detecting an extension product generated using the oligonucleotide as a primer.

25. The method of claim 20, wherein the terminal nucleotide of each oligonucleotide of a pair of oligonucleotides is complementary to a different nucleotide at position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, or a complement thereof.

26. The method of claim 22, wherein the oligonucleotide is any one of SEQ ID NO:4879 to 9736 or SEQ ID NO:64914 to 64922.

27. The method of claim 18, wherein the polynucleotide is contacted with a pair of oligonucleotides each comprising a different detectable label.

28. An isolated polynucleotide comprising at least 50 contiguous nucleotides of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the polynucleotide is less than or equal to about 500,000 nucleotides in length.

29. The isolated polynucleotide of claim 28, wherein the polynucleotide comprises 100 contiguous nucleotides of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895.

30. The isolated polynucleotide of claim 28, wherein the polynucleotide comprises any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895.

31. The isolated polynucleotide of claim 29, wherein the polynucleotide further comprises a detectable label at a position corresponding to position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895.

32. An isolated oligonucleotide that binds to any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the oligonucleotide is at least 10 nucleotides in length.

33. The oligonucleotide of claim 32, wherein the oligonucleotide is any one of SEQ ID NOS:4869 to 19472 or SEQ ID NOS:64896 to 64922.

34. The isolated oligonucleotide of claim 32, wherein the oligonucleotide is at least 15 nucleotides in length

35. A primer pair that binds to a first target region and a second target region of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the a first primer of the primer pair and a second primer of the primer pair are at least 10 nucleotides in length and bind opposite strands of the target region, and prime polynucleotide synthesis from the target region in opposite directions across position 300 of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895.

36. The primer pair of claim 35, wherein the primer is a forward primer and a reverse primer listed in Table 6.

37. An isolated oligonucleotide comprising 10 nucleotides, that selectively binds to a target polynucleotide of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein a terminal nucleotide of the isolated oligonucleotide binds to position 299, 300, or 301 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895.

38. The isolated oligonucleotide of claim 37, wherein the oligonucleotide is at least 15 nucleotides in length.

39. The isolated oligonucleotide of claim 37, wherein the terminal nucleotide binds to position 300 of any one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895.

40. The isolated oligonucleotide of claim 37, wherein the oligonucleotide is any one of SEQ ID NO:4879 to 9736 or SEQ ID NO:64914 to 64922.

41. An isolated vector comprising a polynucleotide of claim 28.

42. An isolated cell comprising the vector of claim 41.

43. A method for sorting bovine subjects, comprising:

a) inferring a breed for a first bovine subject from a nucleic acid sample of the first bovine subject, by a method comprising identifying a nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with the breed; and

b) sorting the first bovine subject based on the inferred breed, and repeating for additional subjects, thereby sorting bovine subjects.

44. The method of claim 43, wherein the bovine subjects are sorted based on whether they are Angus, Limousin, Brahman, Simmental, Hereford, Gelbvieh or Charolais cattle.

45. A method for breeding a bovine subject, comprising:

a) inferring breed of a bovine candidate for use in breeding programs from a nucleic acid sample of the bovine candidate by a method comprising identifying the nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with breed; and

b) determining whether to select the individual for use in breeding programs based on the inferred breed, thereby breeding the bovine subject.

46. The method of claim 45, wherein the selection is implemented at the elite or breeding nucleus level or at the multiplier or foundation animal level.

47. The method of claim 45, wherein the selected bovine subject is used for breeding.
48. A bovine subject resulting from the selection and breeding according to claim 45.
49. The method of claim 48, wherein the selected bovine subject is used for cloning.
50. A method of providing labeling accuracy for breed identified meat products, comprising:
- a) inferring breed of a bovine candidate for use in branded meat products from a nucleic acid sample of the bovine candidate by a method comprising identifying the nucleotide occurrence of at least one single nucleotide polymorphism (SNP) corresponding to position 300 of at least one of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with breed; and
 - b) determining whether to brand the harvested product based on the inferred breed, thereby providing labeling accuracy for breed identified meat products.
51. The method of claim 50, wherein the inferred breed is Angus, Limousin, Brahman, Simmental, Hereford, Gelbvieh or Charolais.
52. A kit for determining nucleotide occurrences or haplotype alleles of bovine SNPs, comprising an oligonucleotide probe, primer, or primer pair, or combinations thereof, for identifying the nucleotide occurrence of at least one bovine single nucleotide polymorphism (SNP) corresponding to position 300 of SEQ ID NOS:1 to 4868 or SEQ ID NOS:64887 to 64895, wherein the SNP is associated with breed.
53. The kit of claim 52, further comprising one or more detectable labels.

54. The kit of claim 52, wherein the kit comprises a plurality of oligonucleotide probes, primers, or primer pairs, or combinations thereof, for identifying the nucleotide occurrence of at least two of the SNPs.

55. The kit of claim 52, wherein the kit comprises at least two probes, primers, or primer pairs for identifying the nucleotide occurrence of at least two SNPs that comprise a haplotype, and wherein the kit allows a determination of a haplotype allele that is associated with the trait.